EMERGING CRYPTIC DISEASES OF FOREST TREES

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DNA based molecular tools have revolutionized the identification of fungi causing diseases of forest trees. This process started almost two decades ago and is still gaining momentum, especially in recent years with advances in next generation sequencing. In many cases, the causal agents of tree diseases have turned out to be a number of morphologically cryptic species, which are sometimes sister taxa, other times not. As a result, the control and management of a number of well-known diseases of trees have had to be re-evaluated. For example, *Botryosphaeria dothidea* and *B. ribis* have long been thought to be the main cause of Botryosphaeria canker on *Eucalyptus* trees around the world. Today it is known that these species are rarely the primary causes of the disease, but that at least 21 other species in the *Botryosphaeriaceae* are also involved, with different species dominating in different regions. Similar examples exist for *Cryphonectria* and *Chrysoporthe*, *Mycosphaerella* and *Teratosphaeria, Fusarium* and many other pathogen groups. This information changes approaches to breed for resistance to these pathogens dramatically. Quarantine programs also need to be re-evaluated to reduce the chances of introducing further diversity in disease causing agents of a particular disease. Another significant challenge lies in understanding and managing the movement of these pathogens between native and non-native trees in a particular region. In this paper we will explore the recent advances in understanding of these cryptic species causing of diseases of forest trees, their origin and potential management.

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